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Result
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Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                            Score
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length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd
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AAB193269
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Arabidopsis thalia
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Streptococcus pneu
Neisseria meningit
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AAG54260 AAG54259 AAG63940 AAAR32076 AAAR32076 AAAR34476 AAAR3452 AAG36453 AAG36451 AAG36451 AAG36451 AAG31022 AAG31022 AAG31022 AAG31022 AAG31026 AAG31065 AAG31065 AAG31065 AAG310666746 ABB581866746 ABB66744 ABB66744	ABG02873 AAM39816 AAM41602 AAE04356 AAE04359 AAY57148 AAG57548 AAG692147 AAB79614 AAR79614 AAR796323 AAW98234 AAG54261
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ALIGNMENTS

RESULT AAB60640 Y CONTRACTOR OF THE CONTRACT O BASB122 protein; strain ATCC43617; antigen; antibody; vaccine; genetic immunisation; infection; upper respiratory tract; otitis media; hearing logs; deafness; pneumonia; sinusitis; nosocomial infection; invasive disease; antibacterial; auditory. 30-JUL-1999; 30-JUL-1999; 31-JUL-2000; 2000WO-EP07365 08-FEB-2001. Moraxella catarrhalis strain ATCC43617 BASB122 protein. 02-MAY-2001 AAB60640; AAB60640 standard; Protein; Thonnard WO200109337-A2. Moraxella catarrhalis. (SMIK) SMITHKLINE BEECHAM BIOLOGICALS J, (first entry) 99GB-0018034. 99GB-0018036. 111 AA

' J

Opacity

WPI; 2001-159874/16. N-PSDB; AAF59778.

New BASB122 and BASB124 polypeptides and polynucleotides from Moraxella

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC invention also relates to immunogenic fragments of the BASB122 and CC invention also relates to immunogenic fragments of the BASB122 and CC BASB124 proteins, expression vectors and host cells comprising BASB122 or CC composition acids, the recombinant production of BASB122 or CC compositions comprising the BASB122 or BASB124 proteins CC compositions comprising an anti-BASB122 or BASB124 proteins CC compositions comprising an anti-BASB122 or BASB124 proteins CC compositions of the invention are useful as prophylactic or therapeutic CC compositions of the invention are useful as prophylactic or therapeutic CC compositions of the invention are useful as prophylactic or therapeutic CC agents against Moraxella catarrhalis infections in mammals, particularly CC isolated from the human upper respiratory tract, which is responsible for CC control of the inventions. It is responsible for about 15% of CC otitis media cases in children (which can lead to temporary or permanent CC enscordial infections and, less frequently, invasive diseases. BASB122 or BASB124 proteins or nucleotides may additionally be used in screening for covel antibacterial compounds, and in the diagnosis and staging of infections and staging of antibacterial compounds, and in the diagnosis and staging of control in the diagnosis and staging 
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Best Local Similarity
Matches 111; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catarrhalis strain ATCC 43617, useful as the
rapeutic agents or vaccines against bacterial infections,
 {\rm e.g.} otitis media or pneumonia \,
  Gilbert CFG,
                                             (MICR-) MICROBIAL TECHNICS LTD
                                                                                          27-JUL-1998;
19-MAR-1999;
                                                                                                                                                            27-JUL-1999;
                                                                                                                                                                                                         10-FEB-2000
                                                                                                                                                                                                                                                      WO200006737-A2
                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                            pneumococcal disease.
                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagno
                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae type 4 protein sequence #82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY81582 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections. The present s
strain ATCC43617 BASB122
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ilarity 100.0%;
Conservative C
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  Hansbro
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                                                                                     98GB-0016337.
99US-0125164.
                                                                                                                                                            99WO-GB02451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                    infection; diagnosis;
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Best Local
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The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful as immunogens detection and diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of 5. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of 8. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumococcal diseases and for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Streptococcal protein, useful as a vaccine, for diagnosis of
                                                        Thonnard
                                                                                                                                                                          03-AUG-2000
                                                                                                                                                                                                     WO200044904-A1
                                                                                                                                                                                                                               Neisseria meningitidis
                                                                                                                                                                                                                                                             bacteraemia;
                                                                                                                                                                                                                                                                         BASB059; respiratory tract infection; invasive bacterial disease;
                                                                                                                                                                                                                                                                                                     Neisseria meningitidis BASB059 protein.
                                                                                                                                                                                                                                                                                                                                                                AAB21107;
                                                                                                                                                                                                                                                                                                                                                                                           AAB21107 standard; Protein; 112 AA
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                                                                                                                29-JAN-1999;
                                                                                                                                             25-JAN-2000;
                                                                                                                                                                                                                                                                                                                                   19-JAN-2001
                                                                                   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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nes 36; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lgalvtavilvtgsvlvilenvtkilhpqpvndegilwlgiiaitinllaslvvgkgktk 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                             meningitis
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                           2000WO-EP00561
                                                                                                                99GB-0002070
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28.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78; DB
Pred. No. 0.36
18; Mismatches
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6;

WPI; 2000-505978/45 N-PSDB; AAA76029.

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Best Local S
Matches 20
                                  The present sequence represents a protein that is specific for pathogenic strains of Neisseria. The polynucleotides, polypeptides, or their antigenic fragments, are used in vaccines to treat or protect against Neisseria infections, particularly by N. meningitidis. The polynucleotide sequence is also used for recombinant production of the polypeptide and to produce attenuated Neisseria strains that overexpress it, or express it in a non-toxic mutant form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the Neisseria meningitidis BASB059 protein. protein, its gene, agonists and antagonists can be used in diagnost assays for the bacterium, as vaccines to prevent infection and as treatments for bacterial infection, particularly those caused by Neisseria meningitidis, such as upper respiratory tract infections, invasive bacterial diseases, bacteraemia and meningitis.
                                                                                                                                                                              Claim 5;
                                                                                                                                                                                                                                                                                                                    Aujame L,
Tinsley C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200026375-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pathogenic strain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a polypeptide of a Neisseria pathogenic strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-2000
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   Sequence
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9908-013,
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12.5%;)	99US-0162142.	99US-0161993.	99US-0161920.	99US-0161361.	99US-0161360.	9905-0161359	99US-0161405.	99US-0161404.	99US-0160989.	9905-0160981	9908-0160815.	99US-0160814.	99US-0160770.	99US-0160768.	99US-0160741.	99US-0159584.	99US-0159638.	99US-U159331.	99US-0159330.	9905-0159329.	9905-0159295.	9908-0159293.	99US-0158369.	9908-0158232.	9905-015/865.	99US-0157753.	99US-0157117.	99US-0156596.	9905-0156458	9908-0155486.	99US-0155139.	99US-0154779.	99US-0154039.	9908-0153758.	9908-0153070.	99US-0152363.	99US-0151438.	99US-0151303.	99US-0151080.	9908-0151065.	99US-0150884.	99US-0150566.	99US-0149902.	99US-0149929.	9908-0149722.	99US-0149426.	99US-0149175.	99US-0148684.	99US-0148565.	9908-0148319.	9908-0148171.	99US-0147493. 99US-0147935.	99US-0147416.	9908-0147260.
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S-0147192. S-0147260. S-0147303. 8-0147416. 8-0147493.

Query Match 12.5 Best Local Similarity 23.5 Matches 36; Conservative

12.5%;

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genetic mapping; gene expression control; promoter;
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06-APR-1999;
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14-MAY-1999;
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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1 Similarity 23.2%;
36; Conservative 2
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990S-013061

990S-0132048

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b; pred. No. 4.7;
26; Mismatches
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                            27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
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10-JUN-1999;
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990S-0144884.
990S-0145085.
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Gaps

Length Indels

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9908-01474933
9908-01474433
9908-0148319
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Matches 17
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Pred. No. 6.8;
18; Mismatches
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12.2%; Score 68; DB 21; Lengt 28.8%; Pred. No. 6.9; 16; Ind ive 18; Mismatches 16; Ind	, , , , , , , , , ,				·
ingth 323; Indels 8; Gaps					
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10-JUN-1999;
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99US-013847.
99US-0139452.
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promoter;
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24-SEP-1999;
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29-SEP-1999;
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Best Local
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26-OCT-1999;
26-OCT-1999;
AAR95910 standard; Protein; 151
                                                                                                                   3 NHHIRLTISALLT----ALLVTGCVS-TGNVA---MKEQNQQTIEQTIIKGKTNKQEIS 53
                                                                                      l Similarity
17; Conserv
                                                                                                                                                        12.2%;
nilarity 28.8%;
Conservative 1
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99US-0149426.
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99US-0150566.
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990S-0151930
990S-0152363
990S-01523758
990S-0154018
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990S-0154039
990S-0154039
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99US-0151303.
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990S-0156458

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990S-0156596

990S-0157753

990S-0157765

990S-0157865

990S-0158232

990S-0158232

990S-0158233

990S-0158233

990S-0159293

990S-0159293
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99US-0159331.
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990S-0160989.
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990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
990S-0161993.
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99US-0160768.
99US-0160770.
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99US-0160815.
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99US-0160741.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0160980
                                                                                                                                                              18;
                                                                                                                                                          Score 68; DB pred. No. 6.9; Nismatches
         AA
                                                                                                                                                                                DB 21;
6.9;
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                                                                                                                                                                                                 Length 325;
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                           RESULT 12
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Opacity associated protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae opacity associated proteins OapA (AAR95909) and OapB (AAR95910) are membrane proteins useful as immunogens in vaccines against typable and non-typable H. influenzae infection. They were identified as the products of 2 open reading frames of an oap gene (AAT27729) isolated from the spontaneous opacity variant an oap gene (AAT27729) isolated from the spontaneous opacity variant H175. Recombinant Oap proteins can be expressed in host cells H175. The combination of the proteins are useful for detecting H. influenzae carrying a vector including an oap gene sequence. Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New opacity associated protein of related DNA, vectors, transformed vaccines and for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-239445/24
N-PSDB; AAT27729.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or for passive immunisation
                                                                                                                                                                                                                                                                                  ABG02873 standard; Protein; 222 AA
                                                                                                                                                                            Novel human diagnostic protein #2864.
                                                                                                                                                                                                                 13-FEB-2002
                                                                                                                                                                                                                                                  ABG02873;
                                                            WO200175067-A2
                                                                                             Homo sapiens.
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                                                                                                                           n; chromosome mapping; gene mapping; gene therapy; forensic supplement; medical imaging; diagnostic; genetic disorder.
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%; Pred. No. 2.9;
10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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Matches

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RRESULT 1

AAM39816

ID AAM3

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KW Huma

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                                                                                                                                                                                                                                                                                                                                                                                                         CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polymcleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess blodiversity
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI:
           Human; nootropic: immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                          Human polypeptide
                                                                                                                            AAM39816
                                                                                                                                                   AAM39816 standard;
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 33232; 103pp; English
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23-AUG-2000;
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                                                                                                   22-OCT-2001
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nes 18; Conserv
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                                                                                                                                                                                                               sqakvqhkev-gtsdwk----lkqflw
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                                                                                                 (first entry)
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates to isolated
                                                                          SEQ
                                                                                                                                                   Protein;
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                                                                                                                                                                                                                                                                                                              Score 66.5; DB Pred. No. 6.4; 18; Mismatches
drug screening;
                                                                          2961.
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Best Local
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14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, and the proposition of the activity cancer diagnosis and therapy, drug screening, and the proposition and thrombolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang
Wang
AAM41602;
                                 AAM41602 standard; Protein; 475
                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAI58972.
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19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                               specification
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                                                                                                                             112
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                                                                                                                                                              71 FGHTAILAPNRWQEIL 86
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                                                                                                                           gghtwvkaigrkaeal 127
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                                                                                                                                                                                                    veagkvaikeshlqstnlthlraivesaenleevvsvlhvfgytdtlgekqtlvvdvvan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for receptor activity, arthritis and
                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                Similarity
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Wang z
Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                               sequence data for this patent did
                                                                                                                                                                                                                                                                                                                                                                          421
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                                                                                                                                                                                                                                                                                Conservative
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2000US-0662191.
2000US-0693036.
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l Z,
u P,
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2000US-0598042.
2000US-0620312.
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Wehrman T,
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                                                                                                                                                                                                                                                                                                11.8%;
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                                                                                                                                                                                                                                                                                                  Score 66;
Pred. No.
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Xu C, Xue
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17;
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a AJ,
RT;
                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                             not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation, leukaemias
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                                                                                                                                                                                                                                                                                29;
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                                                                                                                                                                                                                                                                                                                 Length 421;
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Zhang J;
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25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0652191.
19-CCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                     Query Match
Best Local
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                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                 The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotide or in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as localised neuropathies and shy-Drager Syndrome. Other uses include the lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic activing, inactivity, cancer diagnosis and therapy, drug screening and thrombolytic activity, cancer diagnosis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT,
Wang J,
Zhao QA,
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N-PSDB; AAI60758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; SEQ ID NO 6533; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                Sequence
                                                            106
                                                                                                                     y Match 11.8%;
Local Similarity 31.6%;
hes 24; Conservative
 166
                                                                                                                                                                                                                                              .N.\hat{\mathbf{S}} disorders.
hte: The sequence data for this patent did not form part of the printed
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                                                                                      VSTGNVAMKEQNQOTIEQT----IIKGKTNKQEISS----RFGSADSIS-----FMIVVIK 70
                           FGHTAILAPNRWQEIL 86
                                                          veagkvaikeshlgstnlthlraivesaenleevvsvlhvfgytdtlgekqtlvvdvvan 165
gghtwvkaigrkaeal 183
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Zhou P,
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                                                                                                                                                                                                   475 AA;
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Wehrman T, X
, Goodrich R,
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                                                                                                                           11;
                                                                                                                             score 66; DB
pred. No. 20;
L1; Mismatches
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Xue AJ,
anac RT;
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20;
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Yang Y,
                                                                                                                                                              22;
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                                                                                                                                  29;
                                                                                                                                                              Length 475;
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Zhang J;
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80 Вр

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48 NKQEISS-RFGSADSISFMIVVIKFGHTAILAPNRWQEILSLIISF

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Indels

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Matches

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RESULT 1
AAE04356
                                                        Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE04356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE04356 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO200146393-A2
                                                                              The present invention relates to nucleic acid molecules encoding aspartate kinase useful in cell transformation and transgenic plant production procedures. Nucleic acid encoding aspartate kinase is useful for producing a transgenic plant, by transforming a plant cell with a chimeric gene comprising nucleic acid encoding aspartate kinase with a chimeric gene comprising nucleic acid encoding aspartate kinase operably linked to a regulatory sequence and regenerating a plant from the transformed plant cell. The present sequence is rdrlf.pk005.f20 (FIS) clone Oryza sativa aspartate kinase.
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                                                                                                                                                                                                                                                                                                                                                   21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                  28-JUN-2001
                                                                                                                                                                                               Claim 21; Page 56-57; 64pp; English.
                                                                                                                                                                                                                     Novel nucleic acid molecules encoding aspartate kinase useful in transformation and transgenic plant production procedures \,
                                                                                                                                                                                                                                                            N-PSDB; AAD08624.
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                                                         Sequence
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Local Similarity 32.6
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                                                                                                                                                                                                                                                                                                    Famodu 00,
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                                                            281 AA;
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                                                                                                                                                                                                                                                                                                                                                      99US-0172944.
              11.6%;
                                                                                                                                                                                                                                                                                                     Thorpe CJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transformation; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FIS) clone aspartate kinase.
  Score 64.5; I pred. No. 15; 2; Mismatches
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                               DB
                               22;
                                 Length
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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     July 30, 2002, 15:35:51; Search time 12.91 Seconds (without alignments) 210.011 Million cell updates/sec
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/cgn2_6/ptodata/2/18a/B_COMB.pep:*
/cgn2_6/ptodata/2/18a/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/18a/Packfiles1.pep:*
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US-08-332-576-3
PCT-US95-11672-3
US-07-895-300A-1
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US-08-651-999A-3
US-09-247-373B-48
US-09-247-373B-48
US-09-238-4812-2
US-08-374-843B-10
US-08-374-843B-10
US-08-905-420-16
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US-08-017-114-19
US-08-017-114-19
US-08-017-114-19
US-08-018-2020-4
PCT-US94-02034-19
US-09-082-920-4
PCT-US94-02034-19
US-08-148-058A-29
US-08-148-058A-29
US-08-478-042-27
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US-08-645-215-27
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9.9	9.9	9.9	9.9	10.0	10.0	10.0	10.0	10.0	10.0	10.0	10.1	10.1	10.1	10.1	10.1	10.1	10.1
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US-08-477-108A-6	US-08-121-714-6	US-08-840-204-3	US-09-248-588-9	US-09-542-331-2	US-08-411-389-2	US-08-510-284-1	PCT-US94-00198-2	PCT-US94-00198-1	US-07-551-531-2	US-09-476-482-6	US-08-477-451-2	US-09-171-969-9	US-08-564-972-1	US-09-348-817A-4	US-08-948-997-4	US-08-107-042-2	US-08-466-604-29
Sequence 6,	Sequence 6,	Sequence 3,	Sequence 9,	Sequence 2,	Sequence 2,	Sequence 1,	Sequence 2,	Sequence 1,	Sequence 2,	Sequence 6,	Sequence 2,	Sequence 9,	Sequence 1,	Sequence 4,	Sequence 4,	Sequence 2,	Sequence 29,
, Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appl1	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli), Appl

ALIGNMENTS

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LENGTH: 151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-576-3
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US-08-332-576-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08332576
Patent No. 5756105
                                                                          Query Match
Best Local
                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                                                                TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Weiser, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Libert
                              11 SALLTALLVTGCVSTGNVAMKEQNQQTIE---QTIIKGKTNK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/332,576
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SLIFTALLMTGCVQNANVTTPQAQKMQVEKVDKALQKGEADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
                                                                            Similarity
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                                                             Conservative
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Vaccines for
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                                                          Score 67.5; Di
Pred. No. 0.31
10; Mismatches
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                                                                       DB
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 47
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                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-07-895-300A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/07895300A Patent No. 5279823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNULLANDON, Rebecca L. NAME: Ralph, Rebecca L. 152
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: CH-5'
REFERENCE/TON INFORMATION:
TELECOMMUNICATION 1000
TOTEDHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Weiser, Jeffrey M. TITLE OF INVENTION: Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3:
FILING DATE: October 31,
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb 1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: Norris
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
                                                                                                                                                                                                        TITLE OF INVENTION: PURIFIED FORMS OF DNase NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                             APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Sliwkowski, Mary B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 SALLTALLVTGCVSTGNVAMKEQNQQTIE---QTIIKGKTNK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                           STREET: 450 FULL CONTROL CONTY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                      Φ
                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                    SLIFTALLMTGCVQNANVTTPQAQKMQVEKVDKALQKGEADR 47
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amino acid
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                                                                                                                                                        460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                         USA
                                                                                                                                                                              Genentech,
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                                                         360 Kb floppy disk
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Pred. No. 0.31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08458367 Patent No. 5783433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
APPLICANT: Sliwkowski, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19920608
FILING DATE: 02-Jun-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/409631
FILING DATE: 22-Mar-1995
PRIOR APPLICATION UNMBER: 08/348284
APPLICATION UNMBER: 08/348284
FILING DATE: 30.No. 5783433-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 DQVS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 IA-----LVQEVRDSHLTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERYLFV--YRP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hensley, Max D.
REGISTRATION NUMBER: 27
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 KNLS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: AM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 SADSISFMIVVIKFGHTAIL------APNRWQEILSLIIS------FLWVKPYRP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 HHHLRMRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLVSYIVQILSRYD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 NHHIRLTISALLTALLVTGCVSTGNVAMK--EONQOTIEQTIIKGKTNKO---EISSREG 57
                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                             APPLICATION NUMBER: US/08/458,367 FILING DATE: 02-Jun-1995
                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: 346 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                  94080
                                                                                                                                                                                                                                                                                                                        California
                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sliwkowski, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PURIFIED FORMS OF DNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/07/895,300A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE:

08/116186

APPLICATION DATA:

07/895300

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US-08-458-367-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENCTH: 346 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Applicati
GENERAL INFORMATION:
APPLICANT: Genent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -US93-05136-1
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Genentech, Inc.
TITLE OF INVENTION: PURIFIED FORMS OF DNase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/8: FILING DATE: 08-Jun-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415/225-3562
                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                               TELEPHONE: 415/225-3562
TELEPHONE: 415/225-3562
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 DQVS 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Johnston, Sean A.
REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: P0747C4
                                                                                           NAME: Johnston, Sean A. REGISTRATION NUMBER: P35,910 REFERENCE/DOCKET NUMBER: 7471
                                                                                                                                                                                                                             APPLICATION NUMBER: PFILING DATE: 19930528 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 SADSISFMIVVIKFGHTAIL------APNRWQEILSLIIS-----FLWVKPYRP 100
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                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NHHIRLTISALLTALLVTGCVSTGNVAMK--EQNQQTIEQTIIKGKTNKQ---EISSRFG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                    94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application PC/TUS9305136
FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inc.
                                                                                                                                                                                                                                                                   PCT/US93/05136
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TYPE: AMINO ACID
TOPOLOGY: linear
PCT-US93-05136-1
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; HYPOTHETICAL: ; FRAGMENT TYPE: US-08-651-999A-3
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US-08-651-999A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 24.2
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08651999A Patent No. 6031088
                                                                                                                                                           TELEX: TWX 710-581-47 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stein C. APPLICANT: Stein C. APPLICANT: APPLICANT: APPLICANT APPLICANT AND USES THEREOF NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
CORRESPONDENCE AMSTER, ROTHSTEIN & EBENSTEIN AND THE APPLICANT AVENUE
                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/65
FILING DATE: MAY 23, 1996
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb
                                                                MOLECULE TYPE
                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 SADSISFMIVVIKFGHTAIL------APNRWQEILSLIIS-----FLWVKPYRP 100
                                               DESCRIPTION:
                                                                             TOPOLOGY:
                                                                                            TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 INCH
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 HHHLRMRGMKLLGALLALLAALLQGAVSLKIAAFNIQTFGETKMSNATLVSYIVQILSRYD 108
                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 NHHIRLTISALLTALLYTGCVSTGNVAMK--EQNQQTIEQTIIKGKTNKQ---EISSRFG 57
                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW YORK
                                                                                                                           399 amino acids
                                                                                                                                                                                           (212) 286-0854 or 286-0082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stefan Somlo and Toshio Mochizuki
/ENTION: POLYCYSTIC KIDNEY DISEASE PKD2 GENE
                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                           IBM PC COMPATIBLE
                                                                                                                                                                                                            (212)
                                                                                                                                                                             710-581-4766
               internal fragment
                                             peptide
                                                                                            single
                                                                                                                                                                                                             697-5995
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Pred. No. 3.4;
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Query Match 10.7 Best Local Similarity 23.9 Matches 26; Conservative

10.7%; Score 59.5; 1 23.9%; Pred. No. 14; Live 14; Mismatches

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Length 399;

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Indels

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                                                                                                                                                                                                         DESCRIPTION:
HYPOTHETICAL: 1
FRAGMENT TYPE:
US-09-385-752-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application Patent No. 6228591 GENERAL INFORMATION:
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                                                                                                                          Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/651,99
FILING DATE: MAY 23, 1996
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REGISTRATION NUMBER: 39,911
                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 286-0854 or 286-0882 TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION NUMBER: US/09/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 ALLTALLVTGCVSTGNVAMKEQNQQTIEQ-----TIIKGKTNKQEISSRFGSADS----
                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
   139
                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                  62
                                                             79 SLATALLASWYDGNPAYGMRAYMNDKVSRSMGIGTIRQVRTKKSEIITLFNKLDSERWID 138
                                                                                           12 ALLTALLVTGCVSTGNVAMKEQNQQTIEQ-----TIIKGKTNKQEISSREGSADS----- 61
                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLATALLASWYDGNPAYGMRAYMNDKVSRSMGIGTIRQVRTKKSEIITLFNKLDSERWID 138
DHTRAVIIEFSAYNAQINYFSVVQLLVEIPKSGIYLPNSWVESVRLIKS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10016
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                                                                                                                                                                                                                                                                                                                          amino acid
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90 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stefan Somlo and Toshio Mochizuki
VENTION: POLYCYSTIC KIDNEY DISEASE PKD2 GENE
VENTION: AND USES THEREOF
SQUENCES: 12
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                                                                                                                                                                                                                                                                                        linear
                                                                                                                                Conservative
                                                                                                                                                                                                                                 internal fragment
                                                                                                                                                                                                                                                            peptide
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                                                                                                                                                  10.7%;
23.9%;
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                                  -ISFMIVV---IKFGHTAILAPNRWQEILSLIIS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/09/385,752
                                                                                                                               %; Score 59.5; DE
%; Pred. No. 14;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           96700/395
                                                                                                                                                                      DB 4;
                                                                                                                                       40;
                                                                                                                                                                     Length 399;
                                                                                                                                         Indels
                                                                                                                                           29;
                                                                                                                                           Gaps
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RESULT

DeMuth,

Donald R

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SOFTWARE: MICROSOFT
SEQ ID NO 48
LENGTH: 229
TYPE: PRT
ORGANISM: SOYBEAN
US-09-247-373B-48
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; Sequence 2, Application US/09238481
; Patent No. 6110704
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                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus aureus US-09-238-481-2
                                RESULT 10
US-08-374-843B-6
Sequence 6, Application US/08374843B
; Patent No. 5726016
; Patent No. 5726016
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APPLICANT: Huang, Jianzhong
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: FabG
FILE REFERENCE: GM10192
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Best Local Similarity
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APPLICANT: O'KEEFE, DANIEL
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBBAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
NUMBER OF SEQ ID NOS: 56
NUMBER OF SEQ ID NOS: 56
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
                                                                                                                                                                                                                                                                             Query Match 10.5%;
Best Local Similarity 23.1%;
Matches 27; Conservative 1
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GENERAL INFORMATION:
APPLICANT: DeMuth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 WEEVGSMQIIDPLKFPATTEWITNFLSHPLIKDSLPPRDKMLVYYHNRK 216
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                                                                                                                                                                      47 TNKQEISSRFGSADSISFMI--VVIKFGHTAILAPN-----RWQEIL 86
                                                                                                                                      1 MKMTKSALVTG-----ASRGIGRSIALQLAEEGYNVAVNYAGSKEKAEAVVEEIKAKG-
                                                                                                                                                                                                                                            6 IRLTISALLTALLVTGCVSTG------NVAM-----KEQNQQTIEQTIIKGK 46
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25.7%; Pred. No. 8.8;
tive 20; Mismatches
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Pred. No. 9.7;
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US-08-374-843B-10
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Patent No. 572601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (215)567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Leary, Kathryn Ph.D.
REGISTRATION NUMBER: 3596
REFERENCE/DOCKET NUMBER: 9596
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
TELEFAX: (215) 567-2991
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100 AMINO ACIDS

17PE: amino acid

STRANDEDNESS: si-
TOPOLOGY:

17
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TITLE OF
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                         APPLICANT: Demuth, Donald F APPLICANT: Lally, Edward T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPDALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                               NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF DISEASES ASSOCIATED WITH ACTINOBACILLUS
TITLE OF INVENTION: ACTINOMYCETEMCOMITANS INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                            113 CRHRP-KPKKSKYF 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 QQTIEQTIIKGKTNKQEISSRFGSADSISFMIVVIKF--GHTAILAPNRWQEILSLIISF 92
                                                                        COUNTRY:
                                                                                               STATE:
                                                                                                            CITY: Philadelphia
                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 LWVKPYRPKNLSFY 106
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                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSTFNDGMLEGEAAKQEVSRTLRSSALLVASAIVIHFKSNFTNLL-----ILSQITQY 112
                                                          19103-2398
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                                                                                           Pennsylvania
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                                                                                                                             E: PANITCH SCHWARZE JACOBS & NADEL,
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27.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57; DB 1; Length 150; Pred. No. 7.6;
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RESULT 12
US-08-905-420-6
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TELEX: 831-494
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
            NAME: Leary, Kathryn Ph.D.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9596-7 (F-1080)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DeMuth, Donald R.
APPLICANT: Laily, Edward T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF DISEASES ASSOCIATED WITH ACTINOBACILLUS
TITLE OF INVENTION: ACTINOMYCETEMCOMITANS INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/374,843
FILING DATE: 18-JAN-1995
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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nes 20; Conserv
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REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 95
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SOFTWARE: PatentIn
                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 19103-2398
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1601 Market Street, CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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). 5861255
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                                                                                                                                                                                                                                                                                                                                                                                                                      Pennsylvania
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(215)567-2991
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-905-420-6
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Best Local S:
Matches 20
                                                                                                                     US-08-905-420-10
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08905420 Patent No. 5861255
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION UMBER: US/08/905,420
APPLICATION: 435
CLASSIFICATION 2435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/374,843
APPLICATION UMBER: US 08/374,843
APPLICATION INFORMATION:
APPLICATION INFORMATION:
APPLICATION UMBER: 36,317
APPLICATION UMBER: 36,317
REGISTRATION UMBER: 36,317
REGISTRATION UMBER: 9596-7 (F-REFERENCE/DOCKET NUMBER: 9596-7 (F-REFERENCE/DO
                                                                                                                                                                                                                                                             TELEFAX: (215)567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acid
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APPLICANT: Lally, Edward T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
TITLE OF INVENTION: OF DISEASES ASSOCIATED WITH ACTINOBACILLUS
TITLE OF INVENTION: ACTINOMYCETEMCOMITANS INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPAtible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 QOTIEQTIIKGKTUKQEISSRFGSADSISFMIVVIKF--GHTAILAPURWQEILSLIISF 92
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                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: 150 amino acids amino acid
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linear
                                                                                                                                                                                                                                                                           150 amino acids
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              10.2%;
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                                                                                                                                                                                                                                                                                                                                                  10:
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              Score 57; DB 2; pred. No. 7.6;
                                                     Length 150;
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TELEX: N/A
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; sequence 19, Application US/08505307; Patent No. 6083691; GENERAL INFORMATION:
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APPLICANT: Deretic, Vojo
APPLICANT: Martin, Daniel W.
APPLICANT: METEOTION OF CONVERSION TO MUCCOLDY IN
TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
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Best Local S
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REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: UTSK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/320-7200
TELEFAX: 512/474-7577
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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STATE: Texas
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ZIP: 77210
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FILING DATE: 19930212
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                                                                                                                                                                                                                                                                                               91 SFL------WVKPYR 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 19; Conserv
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pred. NO. 11;
13; Mismatches 12; Indels
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/017,114

FILING DATE: 12-FEB-193

ATTORNEY/AGENT INFORMATION:
NAME: HODGINS, DANIE! 31,026
REGISTRATION NUMBER: UTSK:231
FELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 193 manno acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: 1inear
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Search completed: July 30, 2002, 15:38:55 Job time: 184 sec
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ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PS-TATE PS-DOS-TATE
STATEMENT PS-TATEMENT PS-T
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ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
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APPLICANT: Martin, Daniel W.
TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCCIDY IN
TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
NUMBER OF SEQUENCES: 23
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STATE: TX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 QEQDQQLVE----
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Result
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Perfect score:
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 Pred. No.
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d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                             72.5
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hypothetical lipoprotein [imported] - Escherichia coli (strain O157:H7, substrain RI C;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: B91067 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Tille: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Cross-references: GB:BA000007; PIDN:BAB36929.1; PID:g13362977; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs3506 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-131 <HAY>

Š 뮹 Ş Matches Query Match Best Local 75 17 LLVTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSADSISFMIVVIKFGHT--19 -----AILAPNRWQEILSLIISF LTLAGCSSVGNQSLKNETQESVKTKIVKGKTTKQDVLASFGEPDSRSLIDGEEQWSYTMY 78 Similarity 29.7 27; Conservative 21.1%; 29.7%; 19; Score 117.5; DB: Pred. No. 4.3e-05. 9; Mismatches 30 92 DB 2; 30; Length Indels 131; 15; Gaps 74 ŗ

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NSQSKATSFIPVVGLLAGGADSQTKSLTVSF

cation efflux system protein [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: H95216
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C;Accession: L; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S on, J.D.; Umayam, L.A.; White, O; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtz, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

T.D.; Peterson, S.; H Radune, D.; Holtzappl

A;Atthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morri A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: H95216 Morris

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-299 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK75929.1; PID:g14973359; GSPDB:GN00164; TIGR:

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A; Experimental & C; Genetics: A; Gene: SP1857
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C;Genetics:
A;Gene: czcD
                     iron(III) dicitrate-binding periplasmic protein [imported] - Anabaena sp. (strain C;species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AH2128 R;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Ir R;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Yasuda, M.; Tab. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tab. DNA Res. 8, 205-213, 2001
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A;Title:.Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Molecule type: DNA
A;Residues: 1-328 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74282.1; PID:917131675; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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A; Status: preliminary
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                                                                             hypothetical protein sll1158 - Synechocystis sp. (strain PCC 6803)
C.Species: Synechocystis sp.
A. Variety: PCC 6803
C.Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C.Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C.Accession: S74868
C.Accession: S74868
C.Accession: Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, C.; Accession: Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, C.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yaso, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yaso, A.; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
A; Gene: NMA
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A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491
A;Reference number: A81775; MUID:20222556
A;Accession: B81969
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A; Residues: 1-112 < PAR>
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A; Accession: S74868
A; Status: preliminary
                     A; Reference number: S74322; A; Accession: S74868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLNHH-IRLTISALLTALLVTGC-VSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSR--- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     67 VVIK 70
                                                                                                                                                                                                                                                                                                                                                                                            64 TVGK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILNYHQIKLILESIITALIVIGCEMSTPNNVTINSVNATSEMRVVKHTMGETKIPLRPQR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVVLGGLDNI 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---FGSADSI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLTISALLTALLVTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSADSISFMI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .; Jagels, ...
. 506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.1%; 31.2%;
                                                     MUID:97061201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:AL157959; NID:g7379120; PIDN:CAB83802.1; PID:g737A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74; DB 2; Length 328 Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 112
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Rajandre
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C:Species: Bacillus subtilis
C:Conte: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
C:Accession: C70078
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueeel Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Fark, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A; Accession: C70078
A.;Accession: C70078
A.;Accession: C70078
A.;Accession: C70078
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C70078
hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Delecule type: DNA
A; Residues: 1-226 <KUN>
A; Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB15945.1; PID:e1184634;
A; Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB15945.1; PID:e1184634;
                                                                                                            T49962

hypothetical protein FBM21.160 - Arabidopsi C;Species: Arabidopsis thaliana (mouse-ear C;Date: 02-Jun-2000 #sequence_revision 02-J C;Accession: T49962

R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson
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C;Superfamily: Bacillus subtilis hypothetical protein yxiP
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                              A; Reference number: Z24493
A; Accession: T49962
                                                                                       R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-138 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ypothetical protein yxip - Bacillus subtilis
;Species: Bacillus subtilis
;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
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                                                                                                                                                                                                                                                                                                                                                                                                                                       IRLTISALLTALLVTGCVSTGNVAM-KEQNQQTIEQTIIKGKTNKQE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTGSGDQLRRFFYGD
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                                                                                                                                                                                                                                                                                                                                                                                 IGLCISLLVTVLVMSACESEGEAQMFADCDQKTVKQTAAKPMSSKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSMLRLKTVSSLLTPLILAGMIGLGDVALHSFLPQTQSTAIAAPPSASQEQIELIIASKG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.8%; 36.2%;
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                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 71.5; DB 2;
Pred. No. 5.2;
3; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.4;
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 72.5; DI
Pred. No. 2.4;
                                                                                                                                                                         -ear cress)
02-Jun-2000 #text_change 02-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                     Mewes, H.W.; Rudd,
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                                                                                                            C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C;Accession: E71663 C;Accession: E71663
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499
A;Accession: E71663
                                                                                                                                                                                                                                                                                                                    protein-export membrane protein secd (secD) RP586 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
A; Cross-references: GB:AJ235272;
                              A; Molecule type: DNA
A; Residues: 1-518 <A
                                                                                 A; Status: preliminary; nucleic acid
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190 VSLLKKG---

WQNIGSLVIKSTMGKPYR 214

10

<AND>

GB:AJ235269; NID:g3861033; PIDN:CAA15031.1; PID:g386

sequence not shown; translation not shown

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Query Match
Best Local Similarity
""+"hes 25; Conserv.
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T40178
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A;Introns: 130/1
C;Superfamily: Escherichia coli ribosomal protein
                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: Z97992; PIDN: CAB10813.1; (A; Experimental source: strain 972h-; cosmid c30D10
                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDB. A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z21910
A; Accession: T40178
                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T40178
R;Wood, V.; Rajandream, M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
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A; Residues: 1-568 <BEV>
                                                                                                                                                                                                                                                            A; Gene: rpl10a-2;
                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-216 < WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                             R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, submitted to the EMBL Data Library, February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60s ribosomal protein L10 - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL;AL353993; GSPDB:GN00063; ATSP:F8M21.160
A;Experimental source: cultivar Columbia; BAC clone F8M21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 KFS-----
                                      150 VKSTIKFQLKKVLCLG-VAVGHVDMAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 TRLLVPSSRIGCILGKGGAIITEMRRMTKANIRILGKENLPKVASDDDEMVQVNFMVLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 KFGHTAILAPNRWQEILSLIISFLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
66 IVVIKEGHTAILAPNRWQEILSLIISFLWVKPYR 99
                                                                       6 IRLTISALLTALLVTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSADSISFM 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TALLV----TGCV-STGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSADSISFMIVVI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200/3; 337/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                              Conservative
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                                                                                                                                                                                                                                                            SPDB:SPBC30D10.18c
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                                                                                                                             12.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.78; 27.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 71; DB
Pred. No. 16;
L4; Mismatches
                                                                                                                             Score 70.5; D
Pred. No. 6.3;
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                                                                                                              Mismatches
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                                                                                                                                            Length
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hypothetical protein HI0230 - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: IO-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000

C;Accession: G64145

C;Accession: G64145

C;Accession: G64145

C;Cayton, R.A.; Kirkness, E.F.; Kerlavage, R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, R;Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, G.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.

Common Sequence Common Commo
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                                                                                                                                                                                   hypothetical protein At2g37660 [imported] - Arabidopsis thaliana hypothetical protein F13M22.16 N;Alternate names: hypothetical protein F13M22.16 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;C;Accession: T92532; E84795 C;Accession: T92532; E84795 Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBI Data Library, June 1998 A;Bereire number: Z14677 A;Reference number: Z14677 A;Accession: T92532 A;Accession
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A; Molecule type: DNA
A; Residues: 1-337 <ROU>
A; Cross-references: EMB
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          EMBL: AC004684; NID: g3236234; PID: g3236248
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Pred. No.
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3; Mismatches
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Pred. No. 12;
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A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487 A;Accession: E84795
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A;Introns: 89/1; 179/3; 192/1; 236/3; 257/2; 298/3
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A; Residues: 1-337 <STO>
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R;Wilson, R.; Favello, A.; Le, T.T.
submitted to the PMBL Data Library, April 1997
submitted to the PMBL Data Library april 1997
A;Bescription: The sequence of C. elegans cosmid
A;Reference number: Z20618
A;Reference number: Z20618
A;Accession: T29418
A;Ression: T29418
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Ressiones: 1-530 < WILL-
A;Ressiones: 
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Introns: 16/1;
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                                                                                                                      CTKLEGKVIKDYGGTFIWSVSWQGYIVSAAFLGGFIFSYPAGVLVDRFSARHILSVAILM
                                                                                                                                                                                                                                                       HIGLSLSCMCNSTAV-ALMNTNNATLVEGTESTILMSILENKTSE---SQELGGGDDGES 99
                                                                                                                                                                                                                                                                                                                HIRLTISALLTALLVTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSAD----
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36; Conserv
                                                                LWVKPYRPKNLSFYLTAK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64/2; 112/3; 344/3; 417/1;
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                                                                                                                                                                                                 -SISFMIVVIK----
             177
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 69; DB pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LSFYLTAKA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                    ---FGHTAILAPNRW--QEILSLIISF 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                         47;
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                                                                                                                                                                                                                                                                                                                                                                                                                   36;
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RESULT 15
E71179
hypothetical protein PH1714 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: E71179
C;Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137
A;Accession: E71179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Gene: gspF
C;Superfamily: secretion protein xcpS
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R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998

A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trace; Reference number: A71570; MUID:99000809

A;Accession: C71499
Search completed: July 30, 2002, 15:39:18 Job time: 127 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA30828.1; PID:g3258145
A;Experimental source: strain OT3
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A;Residues: 1-391 <ARN>
A;Cross-references: GB:AE001327; GB:AE001273; NID:g3328999; PIDN:AAC68172.1; PID:g332901
A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable gen. secretion protein F - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-405 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 LIEALTLGCEAVSQDFLREELQEVI-QAVVRGGSLSRELSHRTWTPKLVIGMVALGEESG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 LTALLVTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSADSISFMI----- 66
                                                                                                                                                                                                                           55 DMAYLGAERAKKELGVKIEY-----MTPKSKEDMVPLLEQLAKSKEYDLLVLVGFLWTTP 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 IRLTISALLTALLVTGCVSTGNVAMKEQNQQTIEQTIIKGKTNKQEISSRFGSADSISF- 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.3%; Score 68.5; 22.5%; Pred. No. 20;
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length: 2000000000
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Gapop 10.0 ,
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558
1 MLNHHIRLTISALLTALLVT......FLWVKPYRPKNLSFYLTAKA
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   GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd
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RIOA_SCHPO
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VID_HAEIN
Y130_ARATH
Y141_PYHIO
OAPB_HAEIN
RIOB_SCHPO
OAPB_HAEIN
RIOB_SCHPO
REI_MCYDA
RY5A_HUMAN
TRPD_SULSO
SECV_CYAPA
V406_MYCPN
RPAI_SULSO
MY5A_RAT
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MY5A_RAT
LOLL_DROME
LOLL_DROME
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SYNP_RAT
UBIA_PROST
MY13_HUMAN
MYH3_RAT
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p42307 bacillus su
014363 schizosacch
092cw# rickettsia
p44585 haemophilus
080934 arabidopsis
059403 pyrococcus
p44416 haemophilus
074836 schizosacch
p71496 mycoplasma
000157 ictalurid h
09y411 homo sapien
p50384 sulfolobus
p25014 cyanophora
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Submitted (JUL-1997) to the EMBL/GENES FOR LI IN S.POMBE.
-!- MISCELLANEOUS: THERE ARE TWO GENES FOR LI IN S.POMBE.
-!- SIMILARITY: BELONGS TO THE L1P FAMILY OF RIBOSOMAL PROTEINS.
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STRAIN-MADRID E;
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Andersson S.G.E., Zomorodipour A.
Sicheritz-Ponten T., Alsmark U.C.
                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision;
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r., Alsmark U.C.M., Podowski R
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-!- SUBUNIT: PART OF THE PROKARYOTIC PRO
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SEQUENCE FROM N.A.

STRAIN=RD / KW20 / ATCC 51907;

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STRAINS-95350630; PubMed=7542800;

MEDLINS-95350630; PubMed=7542800;

File Schmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E. M., Brandon R.C.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.;

Whole-genome random sequencing and assembly of Haemophilus
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pF02355; SecD_SecF;
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32, Last sequence up
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                                                                                                            Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Strebphyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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TIGR; HI0230; -
                                             "Sequence and analysis of chromosome thallana.";
                                                                                                Venter J.C.;
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MEDLINE-20083487; PubMed-10617197;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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FUNCTION: MAY BE INVOLVED IN CELL
SUBCELLULAR LOCATION: Attached to
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SUBCELLULAR LOCATION: Chloroplast (Potential)
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SEQUENCE
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                                                                                                                                                                                       "Complete sequence and gene organization thermophilic archaebacterium, Pyrococcus DNA Res. 5:55-76(1998).
                                                                                                                                                                                                                              Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., O
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N.
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikosh
Masuchi Y., Shizuya H., Kikuchi H.;
                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical lipo
PH1714 OR PHAM037
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                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                   Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A.,
                                                                                                                                                                                                                                                                                                                  MEDLINE-98344137;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota;
NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus horikoshii.
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           EMBL; AP000007;
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(Rel. 40, Last annotation update)
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PROTEIN AT2G37520.
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Pred. No. 4.9;
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Matches 27
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MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.!

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.N.

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.N.

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Sprigs T., Hedblom E., Cotton M.D.,

Weidman J.F., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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01-NOV-1995
01-NOV-1995
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prosite; ps00013; prokar_Lipoprotein;
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01-NOV-1995 (Rel. 32,
16-OCT-2001 (Rel. 40,
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Mol. Microbiol. 17:555-564(1995).
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MEDLINE-96100454; PubMed-8559074;
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EMBL; U32718;
TIGR; HI0331;
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                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                         Science 269:496-512(1995).
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                                                                                                                                          modified and this statement is not removed.
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                                     AAA56762.1; -.
AAC21993.1; -.
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074836;
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Eukaryota; Fungi; Ascomycota; Schizosacch
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NCBI_TaxID=4896;
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-i- MISCELLANEOUS: THERE ARE TWO GENES FOR LI IN S.POMBE.
-i- SIMILARITY: BELONGS TO THE L1P FAMILY OF RIBOSOMAL PROTEINS.
RF1_MYCCA
P71496;
01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pfam; pF00687; Ribosomal_L1; 1.
probom; pB0001314; Ribosomal_L1; 2.
proscrib; ps01199; RIBOSOMAL_L1; 1.
Ribosomal protein; Multigene family seQUENCE 216 AA; 23917 MW; D99F
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Q00157;
01-DEC-1992;
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA unclassified Herpesviridae. NCBI_TaxID=10401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene
                                                                                          "Channel catfish virus: a new type Virology 186:9-14(1992).
                                                                                                                     Davison A.J.
                                                                                                                                  MEDLINE-92087490;
                                                                                                                                                STRAIN-AUBURN
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                              Ictalurid herpesvirus 1 Viruses; dsDNA viruses,
                                                                                                                                                                                                                                           Hypothetical 58.
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Pfam; PF00472; RF-1; 1.
PROSITE; PS00745; RF_PROK_I; 1.
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"Cloning of the Mycoplasma capricolum
release factor.";
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2 169:101-103(1996).

2 169:101-103(1996).

5 FUNCTION: PEPTIDE CHAIN RELEASE FACTOR 1 D:
OF TRANSLATION IN RESPONSE TO THE PEPTIDE (
CODONS UAG AND UAA (BY SIMILARITY).

CODONS UAG LOCATION: CYtoplasmic.
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ilarity 26.3%;
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                                                                                                                                  PubMed-1727613;
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Nat. Genet.
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097411; 09UE31; 007902; Q16249; 060653;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin Va (Myosin 5A) (Dilute myosin heavy chain, non-muscle)
                                                                                                                                                                                                              Engle L.J., Kennett R.H.; "Cloning, analysis, and chromosomal localization the human homologue to the mouse dilute gene."; Genomics 19:407-416(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pastural E., Barrat F.J., Dufourcq-Lagelouse R., Certain S., Sanal Jabado N., Seger R., Griscelli C., Fischer A., de Saint Basile G.; "Griscelli disease maps to chromosome 15q21 and is associated with mutations in the myosin-Va gene.";
Nat. Genet. 16:289-292(1997).
                                                                                                                                                                                                                                                                                                    TISSUE=Fetal brain;
MEDLINE=94245227; P
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  Cytogenet.
[6]
                                           Jenkins N.A.; "Cloning and regional assignment of the human (MYH12) gene to chromosome band 15q21.";
                                                                                                               Moore K.J., Testa
                                                                                                                               MEDLINE-95136715;
                                                                                                                                                          TISSUE-Brain
                                                                                                                                                                            SEQUENCE OF 1061-1498 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 638-1477 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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                                                                                                          PubMed=7835087;
J.R., Francke U
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Basile G.;
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pfam; pF01843; DIL; 1.
pfam; pF00612; IQ; 6.
pfam; pF00063; myOsin_head; 1.
pfam; pF00063; myOsin_head; 1.
pR.NTS; pR00193; mYOSINHEAVY.
proDom; pD000355; myOsin_head; 1
proDom; pD00376; DIL; 1.
SMART; SM00011; IQ; 6.
SMART; SM000142; MYSS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1358-1460 FROM N.A. (ISOFORM 3). Edgar A.J., Bennett J.P.; ranshibition of dendrite formation in melanocytes transic transfected with antisense DNA to myosin V."; submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 400:590-593(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mehta A.D.,
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InterPro; IPR000048;
InterPro; IPR001609;
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                                                                                                          Myosin;
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IN 400:590-593(1999).

REPEAT OF THE ACTIN FILAMENT STEPS APPROXIMATING THE 36-NM PSEUDO-REPEAT OF THE ACTIN FILAMENT MAY BE INVOLVED IN MELANOSOME TRANSPORT, OR ALTERNATIVELY, IT MAY BE PROHITED FOR SOME POLARIZATION PROCESS INVOLVED IN DENDRITE
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SUBUNIT: MAY BE A HOMODIMER, WHICH ASSOCIATES WITH MULTIPLE
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                                                                                                                                                                                                                                                                                 ; U90942; AAD00702.1; ...
; Y07759; CAA69035.1; ...
; Y07759; CAA69036.1; ...
; Z22957; CAA80533.1; ...
; S74799; AAB33211.1; ...
; AF055459; AAC14188.1; ...
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160777; -.
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                                                                                                           Repeat; ATP-binding;
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yg; Calmodulin-binding; Actin-binding;
.on; Alternative splicing; Polymorphism.
MYOSIN HEAD-LIKE.
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IQ 2.
IQ 3.
IQ 4.
IQ 5.
IQ 6.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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STRAIN-ATCC 35092 / DSM 1617 / P2;
STRAIN-ATCC 35092 / DIMMed-11427726;
MEDLINE-21332296; PubMed-11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Pen
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina T.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Charlebois R.L., Doolittle W.F., Duguet M., Gasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the Crenarchaeon Sulfolobus solfataric
"The complete genome of the Crenarchaeon Sulfolobus solfataric
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-DSM 5833 / MT-4;
Tutino M.L., Cubellis M., Sannia G., Marino G.;
"The tryptophan operon in Sulfolobus solfataricus.";
submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sulfolobus solfataricus.
Archaea; Crenarchaeota;
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                                                                    CHARACTERIZATION, AND CKXSIALL.
CHARACTERIZATION, AND CKXSIALL.
MEDIINE=21195237; PubMed=11298741;
Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner
Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner
Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner
Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner
Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner
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Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner
Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner
Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner
Ivens A., Mayans O., Szadkowski H., Wilmanns M., Kirschner
Ivens A., Mayans A., M
  SEQUENCE FROM N.A.
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(Rel. 40, Last annotation update)
e phosphoribosyltransferase (EC 2.4.2.18).
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F -> L (IN REF. 1)

MISSING (IN REF. 1)

E -> G (IN REF. 1)

H -> R (IN REF. 1)

V -> L (IN REF. 5)

E -> Q (IN REF. 5)

NIPRKEKDFQGML -> 1

A)

N (IN REF. 5)

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ATP (POTENTIAL)
ACTIN-BINDING (
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Pred. No. 72;
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Matches
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EMBL; AE006710; AAK41173.1; -.
InterPro; IPR000312; Glycos_transf_3.
Pfam; PF00591; Glycos_transf_3; 1.
Pfam; PF02885; Glycos_trans_3N; 1.
ProDom; PD001864; Glycos_transf_3; 1.
Tryptophan blosynthesis; Transferase; Gl
                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-91117189; PMichalowski C.B., PMichalowski S10 s
                                                                                                                                                                                                                                                                                                                                                            SECY_CYAPA
P25014;
01-MAR-1992
Loeffelhardt W., Stirewalt V.L.,
Farley J.Y., Schluchter W.M., Chu
Steiner J.M., Jakowitsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 CYAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 345 AA;
                                                                                                                                                                                                                                                        Eukaryota; Glaucocystophyceae; NCBI_TaxID=2762;
                                                                                                                                                                                                                                                                                                             Preprotein SECY.
                                                         SEQUENCE FROM N.A.
                                                                                                           Bryant D.A.;
                                                                                                                   Stirewalt V.L., Michalowski C.B., Loeffelhardt
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    Cyanelle
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SIMILARITY:
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                                                                                                                                                                                            ; PubMed=2126059;
, Pfanzagl B., Loe
O spc ribosomal pr
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Last annotation update)
                                                                               of the cyanelle DNA 13:327-332(1995).
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Pred. No. 13;
21; Mismatches
                                                                                                                                                                                                                                                                                                                       subunit.
       Chung S., Ne
Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                        i9;
Loeffelhardt W., Bonu
                                                                                                                                                                                                                                                                       Cyanophoraceae;
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                                Michalowski C.B.,
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              Newmann-Spallart C.,
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-ANTCC 29:42 / M129;

C STRAIN-STATO-50:77562; PubMed-8604303;

WAEDLINE-96177562; PubMed-8604303;

RA Hilbert H., Himmelreich R., Plagens H., Herrmann R.;

RT "Sequence analysis of 56 kb from the genome of the bac

RT Mycoplasma pneumoniae comprising the dnaA region, the

Cluster of ribosomal protein genes.";

Cluster of ribosomal protein genes.";
                B
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              Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0303; SECYTRNLCASE.
PROSITE; PS00755; SECY_1; 1.
PROSITE; PS00756; SECY_2; 1.
Protein transport; Transmembrane; Cyanelle; Translocation.
SEQUENCE 492 AA; 55926 MW; 8736219112EBFCOD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plagens
                                                                                                                                                                                                                                                                               Mycoplasmataceae;
NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                           Mycoplasma pneumoniae
Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Y406_
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                                         pneumoniae.
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             SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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12; Conser
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Res. 24:4420-44451....,
AR LOCATION: Integral membrane
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                                                                                                                                                                                                                                                                                                 Mycoplasma
                                                      analysis
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homolog (C12_orf157L)
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                                                        of the
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              protein
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RP STRAIN-ATCC 35092 DSM 1617 / P2;

RX MEDLINE-21312296; PubMed=11427726;

RX MEDLINE-21312296; PubMed=11427726;

RX She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

RA Awayez M.J., Chan-Meiher C.C.-Y., Clausen I.G., Curtis B.A.,

RA Awayez M.J., Chan-Meiher C.C.-Y., Clausen I.G., Curtis B.A.,

RA Awayez M.J., Chan-Meiher C.C.-Y., Clausen I.G., Curtis B.A.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

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RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Heikamp-de Jong I., Jeffries A.C., Lander G., Jeffries A.C., Jeffries
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TRANSMEM 112 132 POTENTIAL.
TRANSMEM 112 132 POTENTIAL.
SEQUENCE 157 AA; 18291 MW; 7D9097A405DAD3C4 CRC64;
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase subunit A' (EC 2.7.7.6).
RPOAL OR SSO0225.
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                                                                                                                         {RNA}(N).
COPACTOR: ZINC (By similarity).
SIMILARITY: THE COMBINED A'+A" SUBUNITS CORRESPOND TO THE SUBUNITS OF EUKARYOTIC RNA POLYMERASES I, II AND III AND TEUBACTERIAL BETA' SUBUNIT.
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        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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157 AA;
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Pred. No. 8;
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Search completed: July 30, 2002, 15:42:00 Job time: 184\ \text{sec}
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                                                                                                                                                                                                                                                                                             Zinc-finger; Complete proteome.
ZN_FING 58 101 C4-TYPE (POTENTIAL).
SEQUENCE 880 AA; 99674 MW; 5C8AE20EFC71DE25 CRC64;
                                                                                                                                                                                                                                                                                                                                              Pfam; PF00623; RNA_pol_A; 1.
Transferase; DNA-directed RNA polymerase;
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                                                                                                                                                   510
                                                                                     557
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                                                                                                                                                  TVKTTLL----TKEEAQQILGVAD------VKIDLGEPAILAPREYYTGKQVISAFL--- 556
                                                                                     ---PKDFNFH 563
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21; Conservative
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: sp_archea:*
2: sp_bacter1a
3: sp_fung1:*
4: sp_human:*
5: sp_inverteb:
6: sp_manumal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
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Match
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558
  562222 seqs, 172994929 residues
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sp_bacteria:*
sp_fungi:*
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                                                                                                                                                                                                                                                      sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_mammal:*
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097nz2 streptococc
09pum2 xenopus lae
0915c3 lactobacill
09jw76 neisseria m
p7377 synechocyst
091xf5 arabidopsis
091u91 human immun
001537 caenorhabdi
09kzz5 streptomyce
000947 tetrahymena
084574 chlamydia t
077772 oryctolagus
094561 arabidopsis
P87977 human immun
09ce58 lactococcus
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45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
65.5	65.5	65.5	65.5	66	66	66	66	66	66.5	66.5	66.5	66.5	66.5	66.5	66.5	67		67	67	67	67	67.5	68	83	68	68	83	83
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	029802 archaeoglob			0	ric	Q9h779 homo sapien	Q9bpx7 homo sapien	O64545 arabidopsis	080245 mycoplasma					Q39162 arabidopsis			O31582 bacillus su	Q9ch57 lactococcus	Q57576 methanococc	Q19553 caenorhabdi		Q9kd84 bacillus ha	mus	9m82 mus	9m81 mus	jizl mus	Q9jlp0 mus musculu	Q9jiz2 mus musculu

ALIGNMENTS

PRELIMINARY: PRT; 299 AA. 097NZ2; 01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-OCT-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 02TION EFFLUX SYSTEM PROTEIN. SP1857. Streptococcus pneumoniae. Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcus. Streptococcus. NCBI_TaxID=1313; [1] SEQUENCE FROM N.A. STRAIN=TIGR4; MEDLINE=-21357209; PubMed=11463916; MEDLINE=-21357209; PubMed=11463916; MEDLINE=-21357209; PubMed=11463916; MEDLINE=-1357209; PubMed=11463916; MEDLINE=-1357209; PubMed=11463916; MEDLINE=-10357209; PubMed=11463916; MEDL
PRT; Created) Last sequ Last anno 4. Last anno 1. Last an

Query Match Best Local Similarity Matches 36; Conserv

Conservative

18;

Score 78; DB 16; Length 299; Pred. No. 2.6; 18; Mismatches 39; Indels

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Gaps

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InterPro; IPR000387; TYR_Prot_ph
InterPro; IPR000242; TYr_Prot_ph
InterPro; IPR000241; fin3; 3.

Pfam; PF00041; fin3; 3.

Pfam; PF001629; MAM; 1.

Pfam; PF001629; MAM; 1.

Pfam; PF001629; MAM; 1.

PFINTS; PR000700; PRTYPHPHTASE.
PRINTS; PR000700; PRTYPHPHTASE.
SMART; SM001060; FN3; 3.

SMART; SM00104; PTPC; 1.

SMART; SM00134; PTPC; 1.

SMART; SM00194; PTPC; 1.

SMART; SM00194; PTPC; 1.

PROSITE; PS00060; MAM; 2; 1.

PROSITE; PS00060; MAM; 2; 1.

PROSITE; PS00080; MAM; 2; 1.

PROSITE; PS00080; MAM; 2; 1.

PROSITE; PS00080; MAM; 3.
Matches
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O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RECEPTOR PROTEIN TYROSINE PHOSPHATASE RHO PRECURSOR (FRAGMENT).
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
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"Xenopus laevis receptor protein tyrosine phosphatase rho.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
EMBL; AF173857; AAD50295.1; -.
HSSP; P28827; 1RPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDILINE-20193505; PubMed-10727868;
MEDILINE-20193505; PubMed-10727868;
Johnson K.G., Holt C.E.;
Johnson K.G., Holt C.E.;
Mexpression of CRYP-alpha, LAR, PTP-delta,
developing xenopus visual system.";
Mech. Dev. 92:291-294(2000).
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Kenopus laevis (African clawed frog).
Fukarvota; Metazoa; Chordata; Craniata; Vertebrata;
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                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                          Glycoprotein;
SIGNAL
                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                          PROSITE;
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  27;
                           Similarity
                                                                                                                                                                                                                                                       PS00740; MAM_1; UNKNOWN_1.
PS50060; MAM_2; 1.
PS00383; TYR_PHOSPHATASE_1; 1.
PS50056; TYR_PHOSPHATASE_2; 1.
PS50055; TYR_PHOSPHATASE_PTP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003961; FN_III.
IPR000998; MAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                    \frac{1195}{1195}
13.4%;
nilarity 30.0%;
Conservative 16
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                                                                                                                                                                                                                       Hydrolase; Signal.
                                                                                                                      1195
AA; 1
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>1195
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Pred.
                                                                                                                                                                            RHO.
                                                                                                                                                                                           RECEPTOR PROTEIN TYROSINE PHOSPHATASE
                                                                                                                                                                                                                       POTENTIAL
            Mismatches
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                                     DB
26;
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               25;
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                                                          Length 1195;
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                 Indels
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       ALD ACCOMMENT OF THE PROPERTY 
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Q9JW76
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Best Local :
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Q9L5C3;
Q9L5C3;
Q1-OCT-2000
Q1-OCT-2000
Q1-DEC-2001
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"Characterization of the collagen-binding S-layer
"Lactobacillus crispatus.";
J. Bacteriol. 182:6440-6450(2000).
EMBL; AF53044; AAF68971.1;
SEQUENCE 458 AA; 48750 MW; 9132CAB6D6A0AD2E CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SURFACE LAYER PROTEIN.
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Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLPNA
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Tankka S., Lounatmaa K., Keranen J.,
Pouwels P.H., Korhonen T.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=IMG 12003;
MEDLINE=20507814; PubMed=11053389;
Medline=20507814; PubMed=11053389;
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STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;
STRAIN-2022556; PubMed=10761919;
MEDLINE-2022556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Chillingworth;
Riee S.R., Morelli G., Basham D., Brown D., Chillingworth;
Riee S.R., Morelli G., Besham D., Brown D., Chillingworth;
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseric meningitidis 22491.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL PROTEIN NMA0510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JW76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MINHHIRLTISALLTALLVTGCVS-----TGNVAMKEONOQTIEQTIIKGKTNKQEI 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Last annotation update)
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Pred. No. 11;
9; Mismatches
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Hook M., West
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Westerlund-Wikstrom
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OT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 62.0 KDA PROTEIN.
GN F8M21_160.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracher Company of the company of 
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Matches
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01-FEB-1997 (TrEMBLrel. 02, Cr
01-FEB-1997 (TrEMBLrel. 02, Le
01-JUN-2000 (TrEMBLrel. 14, L.
01-JUN-2010 (TrEMBLREL) 14, Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okum Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA Res. 3:109-136(1996).
EMBL, D90909; BAA17829.1; -
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EMBL; AL162753; CABB3802.1; -.
Hypothetical protein; Complete
SEQUENCE 112 AA; 11515 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechocystis sp. (strain PCC 6803)
Bacteria; Cyanobacteria; Chroococca
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete SEQUENCE 138 AA; 14585 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-97061201;
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MBLrel. 02, Last seque
MBLrel. 14, Last anno
6 KDA PROTEIN.
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Pred. No. 4.
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7753B6310931D13C
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E5A9D201BF1D168A CRC64;
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                                                             a; Tracheophyta;
eudicots; Rosidae;
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., Yasuda M.,
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Q9IU91;
Q9IU91;
O1-CCT-2000 (TrEMBLrel. 15, Created)
O1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TREMBLREL. 19, Last annotation update)
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                  AIDS Res. Hum. Retroviruses
EMBL; AJ389751; CAB77485.1;
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; pF00013; KH-domain; 4.
SMART; SM00322; KH; 4.
PROSITE; PS50084; KH_TYPE_1;
Hypothetical protein.
SEQUENCE 568 AA; 62034 MW;
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Submitted (APR-2000) to the
EMBL; AL353993; CAB89337.1;
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Rudd s
                                                                                                                                                                                                                                                                                                                                                           "Predominance of subtype A and G HIV type 1 in Nigeria, geographical differences in their distribution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-96NG-MACSW031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; Retroid viruses; NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Peeters M., Esu-Williams E.,
Mulanga-Kabeya C., Harry T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20179113; PubMed=10716369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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InterPro; IPR004088; KH_TYPE_1.
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                            Delaporte E.;
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  120
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                                        HHIRLTISALLTALLVTGCVSTGNVAMKEON-----
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                                                                                  th 12.5%; Similarity 21.2%; 25; Conservative 2
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23; Conservative
                                                                                                                                                                                                                                                    protein; Glycoprotein
                                                                                                                                                                                          328
328 AA;
-TQLLLNGSLAEEDIVIRTENYTDNAKIIIVQLNETIEINCTRPNNNTRK
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36504
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Mayer K.F.X
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27.18;
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he EMBL/GenBank/DDBJ
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                                                                                Score 69.5; D
Pred. No. 23;
29; Mismatches
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Pred. No. 30;
[4; Mismatches
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Ibironke
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                                                                                                                                                                                                                                                                                                                                                                                                              e L.,
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                                                                                                                            15;
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                                                                                  Gaps
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01-DEC-2001
01-DEC-2001
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae; NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular epidemiology of HIV-1 in Portugal: subtypes in Lisbon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               001537;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HYPOTHETICAL 58.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-2000) to the EMBL; AJ296262; CAC82697.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canas-Ferreira W.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Esteves A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2:
Wilson R., Favello A., Le T.
"The sequence of C. elegans
Submitted (APR-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              001537
                                                                                                                                                                                                                                                                           STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
    SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                            None;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SISEGPGQAFYATGDIIGNIRKAHCTI---NRTEWEKMIQNVTQKL--KETFKKNITF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SISF------MIVVIKFGHTAILAPNR--WQEILSLIISFLWVKPYRPKNLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGIKPVVS---TQLLLNGSLAEGNITIRSENITNNAKTIIVQLKEAVNITCIRPSNNTRK 98
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32; Conserv
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[ (TrEMBLrel.
[ (TrEMBLrel.
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168 *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                       Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
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                                                                                                              Le T.T.;
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Last annotation update)
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Pred. No. 12;
20; Mismatches
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                                                                        cosmid F21F8.";
EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venenno T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     530
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12;
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on update)
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                                                                            databases
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                                                                                                                                                                                                                          Consortium.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
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Best I
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"Direct Submission.";
"Direct Submission.";
"Direct Submission.";
"Simited (Aug-2001) to the EMBL/GenBank/DDBJ databases.
subcellular LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
-!- SUGAR TRANSPORTER FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
PUTATIVE INTEGRAL MEMBRANE
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MEDLINE=97000351; PubMed=8843436;
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Cerdeno A.M., Parkhill J., E
Submitted (APR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oliver
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                                                                                                                                                                                                                                                the 8 mb Streptomyces coelicolor A3(2) chromosom Mol. Microbiol. 21:77-96(1996).
EMBL, AL353815; CAB88438.1;
InterPro; IPR000556; Lipocln_cytFABP.
PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
SEQUENCE 169 AA; 18814 MW; B7685780EC402D77
                                                                                                                                                                                                                                                                                                                                                                                                                               Redenbach M., Kieser H.M., Der
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2000)
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                                                                                                                                                          Match
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LTISALLTALLV--TGCVSTGNVAMKEONQQTIEQTIIKGKTNKQE-----ISSRFGSA
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30; Conser
                                                                                                                             Similarity
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nilarity 24.0%;
Conservative 2
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15,
17,
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Pred. No. 45;
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barrell B.G., Rajandream M.A.;
e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Denapaite
                                                                                                      20;
                                                                                                  Score 68.5; Depred. No. 14; No. 14; Mismatches
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45;
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O00947;
O1-JUL-1997 (TrEMBLrel. 04, C
O1-DEC-2001 (TrEMBLrel. 19, L
TETRASKELETAL (FRAGMENT).
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O84574;
O1-NOV-1998 (TrEMBLrel. 0
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O1-DEC-2001 (TrEMBLrel. 1
GEN. SECRETION PROTEIN F.
GSPF OR CT570.
Chlamydda trachomatis.
Bacteria; Chlamydiales; C
NCBI_TaxID-813;
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Submitted (MAY-1997) to the EMBL/Ger
EMBL; AF003091; AAB61407.1; -.
Interpro; IPR003015; HLH_Myc.
PROSITE; PS00038; HELIX_LOOP_HELIX;
                                                                                                                                                                                    Science 282:754-759(1998).

EMBL: AB001377; AAC68172.1; -.

Interpro: IPR001992; Bact_secr_systII.

Pfam: PF00482; GSPII_F; 1.
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-D/UW-3/CX;
MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.
Mitchell W.P., Olinger L., Tatusov
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Query Match
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A. Miranda Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen, Palm C.J., Kamiya A., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
-!-SIMILARITY: BELONGS TO THE SERPIN FAMILY.
EMBL; AF074325; AAC62632.1; -.
HSSP; P05121; 1A7C.
InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE PLASMINOGEN ACTIVATOR INHIBITOR-1 (FRAGMENT).
Oryctolagus cuniculus (Rabbit).
Curative putasyota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Chord
                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eveurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serpin.
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Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                             UNKNOWN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yin J., Idell S.;
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Pred. No. 17;
L3; Mismatches
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annotation update)
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17;
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                                                                    A., Kawai J.,
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RESULT 15
P87977
ID P87977
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AC P87977
DT 01-MAY
DT 01-DE
CENVELL
GN ENVELL
GN Virus
OX Human
OC Virus
OX WCBI.
RN [1]
RP SEQU
RA Xin
RT Who
RI Sub
RN [2]
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Best Local Similarity 28.8
Matches 17; Conservative
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Search completed: July 30, 2002, 15:42:33 Job time: 217 sec
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P87977;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ENVELOPE GLYCOPROTEIN, V1-V5 REGION (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Comparison of HIV-1 env (V1-V5) sequences from dorsal root ganglia "Comparison of HIV-1 env (V1-V5) sequences from dorsal root ganglia with sequences from brain, blood, CSF, and spinal cord from patients who died with AIDS."; submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases. EMBL; U25257; AAB39463.1; ... InterPro; IPR000777; GP120. pfam; PF00516; GP120; 1. ALDS; Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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NON_TER
SEQUENCE
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                                                                                                                                                       GVHLGPGSAFYTTGEVIGDIRRGHCNISRPN-WTNTLGQIAGKLRVQ 243
                                                                                                                                                                                                               EISSRFGSA-DSISEMIVVIKFGHTAILAPNRWQEILSLIISFLWVK 96
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39682 MW; 96AD9399192EA9AA CRC64;
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RESULT
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Match Length DB
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/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985 DAT:

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985 DAT:

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987 DAT:

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1987 DAT:

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989 DAT:

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990 DAT:

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990 DAT:

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992 DAT:

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993 DAT:

/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995 DAT:
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Gapop 60.0 ,
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111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLNHHIRLTISALLTALLVT.....FLWVKPYRPKNLSFYLTAKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.
/SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
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                                                                                                                                                                                                                                                                                   22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the total
                                                                                                                                                                                                                                                                                   AAB60640
                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   distribution.
                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                Moraxella catarrha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    being printed,
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AAB60640;

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The invention relates to the Moraxella catarrhalis strain ATCC43617
CC BASB122 and BASB124 proteins (AAB60640 and AAB60641, respectively)
CC and to DNA encoding them (AAB60640 and AAB60641, respectively). The
CC invention also relates to immunogenic fragments of the BASB122 and comprising the BASB124 proteins, expression vectors and host cells comprising BASB122 or
CC BASB124 proteins, expression vectors and host cells comprising BASB122 or
CC on BASB124, vaccine compositions comprising the BASB122 or BASB124 proteins
CC on compositions comprising an antibody against BASB122 or BASB124, therapeutic
CC compositions comprising an anti-BASB122 or BASB124 proteins
CC compositions comprising an anti-BASB122 or BASB124 proteins
CC detection of BASB122 or BASB124 proteins or anti-BASB124 proteins or compositions of the invention are useful as prophylactic or therapeutic
CC agents against Moraxella catarrhalis infections in mammals, particularly
CC isolated from the human upper respiratory tract, which is responsible for several pathological conditions. It is responsible for about 15% of cities media cases in children (which can lead to temporary or permanent hearing loss). It also causes pneumonia in elderly people, and sinusitis, noscocmial infections and, less frequently, invasive diseases. BASB122 or BASB124 proteins or nucleotides may additionally be used in screening for infections. The present sequence represents the Moraxella catarrhalis cc strain ATCC43617 BASB122 protein.
                     Query Match
Best Local
      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New BASB122 and BASB124 polypeptides and polynucleotides from Moraxella catarrhalis strain ATCC 43617, useful as therapeutic agents or vaccines against bacterial infections, e.g. otitis media or pneumonia \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-1999;
30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASB122 protein; strain ATCC43617; antigen; antibody; vaccine; genetic immunisation; infection; upper respiratory tract; otit hearing loss; deafness; pneumonia; sinusitis; nosocomial infec
                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 66; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF59778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-159874/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2000; 2000WO-EP07365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200109337-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moraxella catarrhalis strain ATCC43617 BASB122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invasive disease; antibacterial; auditory.
                   Local
                     Similarity
                                                                                                       111 AA;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99GB-0018034
99GB-0018036
100.0%; Score 111; DB 22; 100.0%; Pred. No. 3.8e-111; rative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sinusitis; nosocomial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                        Length 111;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tract; otitis media;
    0;
    Gaps
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Search completed: July 30, 2002, 15:43:08 Job time: 227 sec

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Page 2

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Title:
Perfect score:
Sequence:
                                                                 Result
No.
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Listing first 1000 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
No matches found
                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                               Query
Score Match Length DB
                                                                                                                                                                                                                                                                Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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Capop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         July 30, 2002, 15:39:51; Search time 13.05 Seconds (without alignments) 207.758 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231628 segs, 24425594 residues
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111
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                                                                                                                                   SUMMARIES
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                                                               Description
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Search completed: July 30, 2002, 15:43:27 Job time: 216 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

Title: Perfect score: Sequence:

US-10-048-197-2 111 1 MLNHHIRLTISALLTALLUT......FLWVKPYRPKNLSFYLTAKA 111

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 283138 segs, 96089334 residues

Word size : 15

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Score Match Length DB ID

Description

No matches found

Search completed: July 30, 2002, 15:43:50 Job time: 124 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 30, 2002, 15:43:31; Search time 11.9 Seconds (without alignments) 361.166 Million cell updates/sec

Title: Perfect score: Sequence: US-10-048-197-2 111 1 MLNHHIRLTISALLTALLVT.....FLWVKPYRPKNLSFYLTAKA 111

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 15

Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Score Match Length DB ID

Description

No matches found

Search completed: July 30, 2002, 15:47:02 Job time: 211 sec

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
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No matches found
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                                              Query
Score Match Length DB
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           July 30, 2002, 15:43:11; Search time 24.65 Seconds (without alignments) 779.004 Million cell updates/sec
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111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MLNHHIRLTISALLTALLVT.....FLWVKPYRPKNLSFYLTAKA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                       sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_rodent:*
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sp_phage:*
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Search completed: July 30, 2002, 15:46:44 Job time: 213 sec

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